

&lt;!--StartFragment--&gt;

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OM protein - protein search, using sw model

Run on: December 27, 2006, 21:00:21 ; Search time 199 Seconds  
 (without alignments)  
 1346.376 Million cell updates/sec

Title: US-10-716-359-16  
 Perfect score: 3104  
 Sequence: 1 MLYLENNNAQTQFSEPQYTNL.....FNFDMDARRNKQQRKEEGE 586

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 500 summaries

Database : A\_Geneseq\_8:\*  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*  
 9: geneseqp2005s:\*  
 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3104	100.0	586	2	AAY05956	Aay05956 Human cel
2	3104	100.0	586	5	ABG95140	Abg95140 Human onc
3	3100	99.9	586	5	ABG95132	Abg95132 Human onc
4	3087	99.5	586	3	AAB11357	Aab11357 Human p63
5	3087	99.5	586	5	ABB74989	Abb74989 Human p53
6	3087	99.5	586	5	ABP61909	Abp61909 Human lun
7	3087	99.5	586	7	ADH36992	Adh36992 Human lun
8	3087	99.5	586	8	ADM56795	Adm56795 Human lun
9	3087	99.5	586	8	ADN04517	Adn04517 Antipsori
10	3087	99.5	586	9	ADU98487	Adu98487 Human p53
11	3087	99.5	586	9	AEB10295	Aeb10295 Cancer re
12	3087	99.5	586	9	AEE06149	Aee06149 p53 tumor
13	3080	99.2	586	2	AAY41032	Aay41032 Human lun
14	3080	99.2	586	3	AAB11317	Aab11317 Human lun
15	3080	99.2	586	5	ABB74949	Abb74949 Human lun

16	3080	99.2	586	5	ABP61869	Abp61869	Human	lun
17	3080	99.2	586	7	ADE53447	Ade53447	Human	lun
18	3080	99.2	586	7	ADH36806	Adh36806	Human	lun
19	3080	99.2	586	8	ADM56609	Adm56609	Human	lun
20	3080	99.2	586	8	ADN89653	Adn89653	Human	lun
21	3080	99.2	586	9	ADU98301	Adu98301	Lung	tumo
22	3080	99.2	586	9	AEB10109	Aeb10109	Cancer	re
23	3080	99.2	586	9	AEE05963	Aee05963	Human	lun
24	3078	99.2	586	7	ADA28428	Ada28428	p53	tumou
25	3077	99.1	586	7	ADA28242	Ada28242	Human	lun
26	3066	98.8	586	2	AAY05962	Aay05962	Mouse	cel
27	3033	97.7	641	2	AAY45247	Aay45247	Human	p51
28	3033	97.7	641	2	AAY05953	Aay05953	Human	cel
29	3033	97.7	641	4	AAB82129	Aab82129	Human	pro
30	3033	97.7	641	5	ABG95142	Abg95142	Human	onc
31	3033	97.7	687	7	ADL22695	Adl22695	Human	dis
32	3029	97.6	641	3	AAB11358	Aab11358	Human	p63
33	3029	97.6	641	5	ABG95136	Abg95136	Human	onc
34	3029	97.6	641	5	ABG95128	Abg95128	Human	onc
35	3029	97.6	641	5	ABB74990	Abb74990	Human	p53
36	3029	97.6	641	5	ABP61910	Abp61910	Human	lun
37	3029	97.6	641	7	ADA28429	Ada28429	p53	tumou
38	3029	97.6	641	7	ADH36993	Adh36993	Human	lun
39	3029	97.6	641	8	ADM56796	Adm56796	Human	lun
40	3029	97.6	641	9	ADU98488	Adu98488	Human	p53
41	3029	97.6	641	9	AEB10296	Aeb10296	Cancer	re
42	3029	97.6	641	9	AEE06150	Aee06150	p53	tumor
43	3025	97.5	680	3	AAY50997	Aay50997	Human	KET
44	3025	97.5	680	3	AAB11361	Aab11361	Human	p63
45	3025	97.5	680	5	ABB74993	Abb74993	Human	p53
46	3025	97.5	680	5	ABP61913	Abp61913	Human	lun
47	3025	97.5	680	7	ADA28432	Ada28432	p53	tumou
48	3025	97.5	680	7	ADH36996	Adh36996	Human	lun
49	3025	97.5	680	8	ADM56799	Adm56799	Human	lun
50	3025	97.5	680	8	ABM80526	Abm80526	Tumour-as	
51	3025	97.5	680	8	ADU06284	Adu06284	Novel	bro
52	3025	97.5	680	9	ADU98491	Adu98491	Human	p53
53	3025	97.5	680	9	AEB10299	Aeb10299	Cancer	re
54	3025	97.5	680	9	AEE06153	Aee06153	p53	tumor
55	2995	96.5	680	2	AAY05958	Aay05958	Human	cel
56	2991	96.4	680	3	AAY50998	Aay50998	Rat	KET p
57	2421	78.0	461	3	AAB11362	Aab11362	Human	p63
58	2421	78.0	461	5	ABG95131	Abg95131	Human	onc
59	2421	78.0	461	5	ABG95138	Abg95138	Human	onc
60	2421	78.0	461	5	ABB74994	Abb74994	Human	p53

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OM protein'- protein search, using sw model

Run on: December 27, 2006, 21:01:02 ; Search time 306 Seconds  
(without alignments)  
1771.435 Million cell updates/sec

Title: US-10-716-359-16  
Perfect score: 3104  
Sequence: 1 MLYLENNNAQTQFSEPQYTNL.....FNFDMDARRNKQQRIKEEGE 586

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3033	97.7	680	1 P73L_HUMAN	Q9h3d4 homo sapien
2	3026	97.5	582	2 Q3UVI3_MOUSE	Q3uvi3 mus musculu
3	3017	97.2	582	2 Q5CZX0_MOUSE	Q5czx0 mus musculu
4	2995	96.5	680	1 P73L_MOUSE	O88898 mus musculu
5	2991	96.4	680	1 P73L_RAT	Q9jjp6 rattus norv
6	2962	95.4	582	2 Q9DEC7_CHICK	Q9dec7 gallus gall
7	2416	77.8	565	2 Q4S122_TETNG	Q4s122 tetraodon n
8	2344	75.5	576	2 Q8JFE3_BRARE	Q8jfe3 brachydanio
9	2330	75.1	588	2 Q8JHZ6_BRARE	Q8jhz6 brachydanio
10	1877	60.5	393	2 Q569E5_MOUSE	Q569e5 mus musculu
11	1826	58.8	457	2 Q8JHZ5_BRARE	Q8jhz5 brachydanio
12	1777	57.2	641	2 Q9W664_BARBU	Q9w664 barbus barb
13	1774	57.2	640	2 Q801Z7_BRARE	Q801z7 brachydanio
14	1771	57.1	640	2 Q6UNX2_BRARE	Q6unx2 brachydanio
15	1748.5	56.3	590	2 Q9JJP1_MOUSE	Q9jjp1 mus musculu
16	1744.5	56.2	631	2 Q9JJP2_MOUSE	Q9jjp2 mus musculu
17	1741	56.1	636	1 P73_HUMAN	O15350 homo sapien
18	1730.5	55.8	365	2 Q98SW0_XENLA	Q98sw0 xenopus lae
19	1720.5	55.4	637	1 P73_CERAE	Q9xsk8 cercopithec
20	1579	50.9	434	2 Q6DG24_BRARE	Q6dg24 brachydanio
21	1562	50.3	514	2 Q9CU77_MOUSE	Q9cu77 mus musculu
22	1507.5	48.6	494	2 Q3UT91_MOUSE	Q3ut91 mus musculu
23	1481	47.7	662	2 Q4S837_TETNG	Q4s837 tetraodon n

24	1464	47.2	555	2	Q5KQU6_BRARE	Q5kqu6 brachydanio
25	1459.5	47.0	497	2	Q9WUJ0_MOUSE	Q9wuj0 mus musculu
26	950.5	30.6	621	2	Q9NGC7_MYAAR	Q9ngc7 mya arenari
27	912	29.4	591	2	Q8T7V3_SPISO	Q8t7v3 spisula sol
28	912	29.4	596	2	Q6WG19_SPISO	Q6wg19 spisula sol
29	912	29.4	596	2	Q6WG20_SPISO	Q6wg20 spisula sol
30	896.5	28.9	564	2	Q27937_LOLFO	Q27937 loligo forb

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OM protein - protein search, using sw model

Run on: December 27, 2006, 21:04:46 ; Search time 41 Seconds  
(without alignments)  
1375.196 Million cell updates/sec

Title: US-10-716-359-16  
Perfect score: 3104  
Sequence: 1 MLYLENNAAQTQFSEPQYTNL.....FNFDMDARRNKQQRIKEEGE 586

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : PIR\_80:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1774	57.2	640	2 JC7989	p73 protein - zebr
2	839.5	27.0	396	1 JH0631	cellular tumor ant
3	762	24.5	363	1 A29376	cellular tumor ant
4	758.5	24.4	367	1 S02193	cellular tumor ant
5	744	24.0	386	1 S51648	cellular tumor ant
6	723	23.3	391	1 S02192	cellular tumor ant
7	712	22.9	396	1 JH0633	cellular tumor ant
8	707.5	22.8	393	1 DNHU53	cellular tumor ant
9	703	22.6	393	1 S06594	cellular tumor ant
10	702	22.6	390	1 DNMS53	cellular tumor ant
11	700	22.6	391	2 JC6193	tumor suppressor p
12	697.5	22.5	393	2 JC6176	tumor suppressor p
13	688.5	22.2	381	2 S38824	cellular tumor ant
14	259.5	8.4	77	2 I46226	cellular tumor ant
15	152.5	4.9	925	2 T19361	hypothetical prote
16	134.5	4.3	901	2 JC6093	dead ringer nuclea
17	133	4.3	1081	2 S66736	transcription acti
18	133	4.3	1520	1 TVFFA	protein-tyrosine k
19	132.5	4.3	2578	2 A56922	transcription fact
20	130.5	4.2	2529	2 A56923	transcription fact
21	129	4.2	963	2 T40290	hypothetical prote

22	129	4.2	964	2	T41547	hypothetical prote
23	129	4.2	1051	2	G59436	KIAA1304 protein [
24	129	4.2	1621	2	T15264	hypothetical prote
25	128.5	4.1	628	2	S19150	hypothetical prote
26	126.5	4.1	628	2	JQ0110	hypothetical 69K p
27	126	4.1	2897	2	B48666	cell proliferation
28	126	4.1	3256	2	A48666	cell proliferation
29	125.5	4.0	628	2	S01955	hypothetical prote
30	125	4.0	724	2	T47149	hypothetical prote

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OM protein - protein search, using sw model

Run on: December 27, 2006, 21:10:02 ; Search time 50 Seconds  
(without alignments)  
1025.859 Million cell updates/sec

Title: US-10-716-359-16  
Perfect score: 3104  
Sequence: 1 MLYLENNNAQTQFSEPQYTNL.....FNFDMDARRNKQQRKEEGE 586

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3104	100.0	586	2	US-09-538-106-16	Sequence 16, Appl
2	3104	100.0	586	3	US-09-529-583-16	Sequence 16, Appl
3	3087	99.5	586	2	US-09-643-597-338	Sequence 338, App
4	3087	99.5	586	2	US-09-542-615A-338	Sequence 338, App
5	3087	99.5	586	2	US-09-606-421B-338	Sequence 338, App
6	3087	99.5	586	2	US-09-630-940B-338	Sequence 338, App
7	3087	99.5	586	2	US-10-007-700-338	Sequence 338, App
8	3080	99.2	586	2	US-09-643-597-152	Sequence 152, App
9	3080	99.2	586	2	US-09-480-884A-152	Sequence 152, App
10	3080	99.2	586	2	US-09-542-615A-152	Sequence 152, App
11	3080	99.2	586	2	US-09-606-421B-152	Sequence 152, App
12	3080	99.2	586	2	US-09-221-107-152	Sequence 152, App
13	3080	99.2	586	2	US-09-466-396A-152	Sequence 152, App
14	3080	99.2	586	2	US-09-476-496A-152	Sequence 152, App
15	3080	99.2	586	2	US-09-630-940B-152	Sequence 152, App
16	3080	99.2	586	2	US-09-285-479-152	Sequence 152, App
17	3080	99.2	586	2	US-10-007-700-152	Sequence 152, App
18	3066	98.8	586	2	US-09-538-106-22	Sequence 22, Appl

19	3066	98.8	586	3	US-09-529-583-22	Sequence 22, Appl
20	3033	97.7	641	2	US-09-538-106-13	Sequence 13, Appl
21	3033	97.7	641	3	US-09-529-583-13	Sequence 13, Appl
22	3029	97.6	641	2	US-09-643-597-339	Sequence 339, App
23	3029	97.6	641	2	US-09-542-615A-339	Sequence 339, App
24	3029	97.6	641	2	US-09-606-421B-339	Sequence 339, App
25	3029	97.6	641	2	US-09-630-940B-339	Sequence 339, App
26	3029	97.6	641	2	US-10-007-700-339	Sequence 339, App
27	3025	97.5	680	2	US-09-643-597-342	Sequence 342, App
28	3025	97.5	680	2	US-09-542-615A-342	Sequence 342, App
29	3025	97.5	680	2	US-09-606-421B-342	Sequence 342, App
30	3025	97.5	680	2	US-09-630-940B-342	Sequence 342, App
31	3025	97.5	680	2	US-10-007-700-342	Sequence 342, App
32	2995	96.5	680	2	US-09-538-106-19	Sequence 19, Appl
33	2995	96.5	680	3	US-09-529-583-19	Sequence 19, Appl
34	2421	78.0	461	2	US-09-643-597-343	Sequence 343, App
35	2421	78.0	461	2	US-09-542-615A-343	Sequence 343, App
36	2421	78.0	461	2	US-09-606-421B-343	Sequence 343, App
37	2421	78.0	461	2	US-09-630-940B-343	Sequence 343, App
38	2421	78.0	461	2	US-09-538-106-17	Sequence 17, Appl
39	2421	78.0	461	2	US-10-007-700-343	Sequence 343, App
40	2421	78.0	461	3	US-09-529-583-17	Sequence 17, Appl
41	2398	77.3	461	2	US-09-538-106-23	Sequence 23, Appl
42	2398	77.3	461	3	US-09-529-583-23	Sequence 23, Appl
43	2350	75.7	516	2	US-09-643-597-344	Sequence 344, App
44	2350	75.7	516	2	US-09-542-615A-344	Sequence 344, App
45	2350	75.7	516	2	US-09-606-421B-344	Sequence 344, App
46	2350	75.7	516	2	US-09-630-940B-344	Sequence 344, App
47	2350	75.7	516	2	US-09-538-106-14	Sequence 14, Appl
48	2350	75.7	516	2	US-10-007-700-344	Sequence 344, App
49	2350	75.7	516	3	US-09-529-583-14	Sequence 14, Appl
50	2327	75.0	555	2	US-09-538-106-20	Sequence 20, Appl

&lt;!--EndFragment--&gt;



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OM protein - protein search, using sw model

Run on: December 27, 2006, 21:21:46 ; Search time 186 Seconds  
(without alignments)  
1459.376 Million cell updates/sec

Title: US-10-716-359-16  
Perfect score: 3104  
Sequence: 1 MLYLENNAAQTQFSEPQYTNL.....FNFDMDARRNKQQRKEEGE 586

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3104	100.0	586	4	US-10-716-359-16
2	3104	100.0	586	5	US-10-469-469-306
3	3104	100.0	586	6	US-11-109-831-16
4	3100	99.9	586	5	US-10-469-469-290
5	3087	99.5	586	3	US-09-735-705-338
6	3087	99.5	586	3	US-09-850-716A-338
7	3087	99.5	586	3	US-09-897-778-338
8	3087	99.5	586	4	US-10-007-700-338
9	3087	99.5	586	4	US-10-117-982-338
10	3087	99.5	586	4	US-10-313-986-338
11	3087	99.5	586	5	US-10-775-972-338
12	3087	99.5	586	5	US-10-922-124-338
13	3087	99.5	586	5	US-10-623-155-338
14	3080	99.2	586	3	US-09-735-705-152
15	3080	99.2	586	3	US-09-850-716A-152
16	3080	99.2	586	3	US-09-897-778-152
17	3080	99.2	586	3	US-09-466-396A-152
18	3080	99.2	586	4	US-10-007-700-152
19	3080	99.2	586	4	US-10-117-982-152

20	3080	99.2	586	4	US-10-313-986-152	Sequence 152, App
21	3080	99.2	586	5	US-10-775-972-152	Sequence 152, App
22	3080	99.2	586	5	US-10-922-124-152	Sequence 152, App
23	3080	99.2	586	5	US-10-623-155-152	Sequence 152, App
24	3066	98.8	586	4	US-10-716-359-22	Sequence 22, Appl
25	3066	98.8	586	6	US-11-109-831-22	Sequence 22, Appl
26	3033	97.7	641	4	US-10-716-359-13	Sequence 13, Appl
27	3033	97.7	641	5	US-10-469-469-310	Sequence 310, App
28	3033	97.7	641	6	US-11-109-831-13	Sequence 13, Appl
29	3029	97.6	641	3	US-09-735-705-339	Sequence 339, App
30	3029	97.6	641	3	US-09-850-716A-339	Sequence 339, App
31	3029	97.6	641	3	US-09-897-778-339	Sequence 339, App
32	3029	97.6	641	4	US-10-007-700-339	Sequence 339, App
33	3029	97.6	641	4	US-10-117-982-339	Sequence 339, App
34	3029	97.6	641	4	US-10-313-986-339	Sequence 339, App
35	3029	97.6	641	5	US-10-775-972-339	Sequence 339, App
36	3029	97.6	641	5	US-10-922-124-339	Sequence 339, App
37	3029	97.6	641	5	US-10-623-155-339	Sequence 339, App
38	3029	97.6	641	5	US-10-469-469-282	Sequence 282, App
39	3029	97.6	641	5	US-10-469-469-298	Sequence 298, App
40	3025	97.5	680	3	US-09-735-705-342	Sequence 342, App
41	3025	97.5	680	3	US-09-850-716A-342	Sequence 342, App
42	3025	97.5	680	3	US-09-897-778-342	Sequence 342, App
43	3025	97.5	680	4	US-10-007-700-342	Sequence 342, App
44	3025	97.5	680	4	US-10-117-982-342	Sequence 342, App
45	3025	97.5	680	4	US-10-313-986-342	Sequence 342, App
46	3025	97.5	680	5	US-10-775-972-342	Sequence 342, App
47	3025	97.5	680	5	US-10-922-124-342	Sequence 342, App
48	3025	97.5	680	5	US-10-623-155-342	Sequence 342, App
49	2995	96.5	680	4	US-10-716-359-19	Sequence 19, Appl
50	2995	96.5	680	6	US-11-109-831-19	Sequence 19, Appl
51	2421	78.0	461	3	US-09-735-705-343	Sequence 343, App
52	2421	78.0	461	3	US-09-850-716A-343	Sequence 343, App
53	2421	78.0	461	3	US-09-897-778-343	Sequence 343, App
54	2421	78.0	461	4	US-10-007-700-343	Sequence 343, App
55	2421	78.0	461	4	US-10-117-982-343	Sequence 343, App
56	2421	78.0	461	4	US-10-313-986-343	Sequence 343, App
57	2421	78.0	461	4	US-10-716-359-17	Sequence 17, Appl
58	2421	78.0	461	5	US-10-775-972-343	Sequence 343, App
59	2421	78.0	461	5	US-10-922-124-343	Sequence 343, App
60	2421	78.0	461	5	US-10-623-155-343	Sequence 343, App

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OM protein - protein search, using sw model

Run on: December 27, 2006, 21:23:46 ; Search time 46 Seconds  
(without alignments)  
1246.430 Million cell updates/sec

Title: US-10-716-359-16  
Perfect score: 3104  
Sequence: 1 MLYLENNNAQTQFSEPQYTNL.....FNFDMDARRNKQQRKEEGE 586

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 390055 seqs, 97842647 residues

Total number of hits satisfying chosen parameters: 390055

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : Published\_Applications\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3033	97.7	641	7	US-11-340-715-4
2	2995	96.5	641	7	US-11-340-715-11
3	1813	58.4	448	7	US-11-340-715-1
4	1746	56.2	587	6	US-10-489-730-2
5	1741	56.1	636	7	US-11-340-715-8
6	1718.5	55.4	661	6	US-10-489-730-11
7	1420.5	45.8	450	6	US-10-489-730-4
8	1415.5	45.6	499	7	US-11-340-715-6
9	1256	40.5	426	6	US-10-489-730-6
10	1046	33.7	312	7	US-11-340-715-7
11	960.5	30.9	349	7	US-11-340-715-9
12	707.5	22.8	354	6	US-10-538-066-763
13	707.5	22.8	393	6	US-10-538-066-367
14	707.5	22.8	393	7	US-11-315-777-9
15	707.5	22.8	393	7	US-11-340-715-3
16	707.5	22.8	393	7	US-11-009-357-6
17	707.5	22.8	393	7	US-11-319-873-9

18	707.5	22.8	393	7	US-11-254-926-9	Sequence 9, Appli
19	707.5	22.8	393	7	US-11-304-280-9	Sequence 9, Appli
20	707.5	22.8	393	7	US-11-239-548-9	Sequence 9, Appli
21	707.5	22.8	425	7	US-11-009-357-2	Sequence 2, Appli
22	702.5	22.6	393	6	US-10-546-829-1	Sequence 1, Appli
23	702.5	22.6	393	7	US-11-404-146-3	Sequence 3, Appli
24	699.5	22.5	393	7	US-11-371-354-72585	Sequence 72585, A
25	316	10.2	102	6	US-10-538-066-765	Sequence 765, App
26	291.5	9.4	100	6	US-10-489-730-12	Sequence 12, Appl
27	285.5	9.2	100	6	US-10-489-730-14	Sequence 14, Appl
28	284.5	9.2	100	6	US-10-489-730-13	Sequence 13, Appl
29	133	4.3	2801	7	US-11-375-359-120	Sequence 120, App
30	133	4.3	2896	7	US-11-375-359-121	Sequence 121, App

&lt;!--StartFragment--&gt;

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: December 27, 2006, 19:24:15 ; Search time 59 Seconds  
(without alignments)  
4094.024 Million cell updates/sec

Title: US-10-716-359-4  
Perfect score: 3260  
Sequence: 1 atgttggtacctggaaaacaa.....tcaaagaggaggggggagtga 1761

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 5179358

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_n2p.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10716359/runat\_27122006\_140406\_325/app\_query.fasta\_1  
-DB=A\_Geneseq -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p  
-USER=US10716359@CGN\_1\_1\_440@runat\_27122006\_140406\_325 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query						
No.	Score	Match	Length	DB	ID	Description	
-----							

1	3104	95.2	586	2	AAY05956	Aay05956	Human	cel
2	3104	95.2	586	5	ABG95140	Abg95140	Human	onc
3	3100	95.1	586	5	ABG95132	Abg95132	Human	onc
4	3087	94.7	586	3	AAB11357	Aab11357	Human	p63
5	3087	94.7	586	5	ABB74989	Abb74989	Human	p53
6	3087	94.7	586	5	ABP61909	Abp61909	Human	lun
7	3087	94.7	586	7	ADH36992	Adh36992	Human	lun
8	3087	94.7	586	8	ADM56795	Adm56795	Human	lun
9	3087	94.7	586	8	ADN04517	Adn04517	Antipsori	
10	3087	94.7	586	9	ADU98487	Adu98487	Human	p53
11	3087	94.7	586	9	AEB10295	Aeb10295	Cancer re	
12	3087	94.7	586	9	AEE06149	Aee06149	p53 tumor	
13	3080	94.5	586	2	AAY41032	Aay41032	Human	lun
14	3080	94.5	586	3	AAB11317	Aab11317	Human	lun
15	3080	94.5	586	5	ABB74949	Abb74949	Human	lun
16	3080	94.5	586	5	ABP61869	Abp61869	Human	lun
17	3080	94.5	586	7	ADE53447	Ade53447	Human	lun
18	3080	94.5	586	7	ADH36806	Adh36806	Human	lun
19	3080	94.5	586	8	ADM56609	Adm56609	Human	lun
20	3080	94.5	586	8	ADN89653	Adn89653	Human	lun
21	3080	94.5	586	9	ADU98301	Adu98301	Lung tumo	
22	3080	94.5	586	9	AEB10109	Aeb10109	Cancer re	
23	3080	94.5	586	9	AEE05963	Aee05963	Human	lun
24	3078	94.4	586	7	ADA28428	Ada28428	p53 tumou	
25	3077	94.4	586	7	ADA28242	Ada28242	Human	lun
26	3066	94.0	586	2	AAY05962	Aay05962	Mouse	cel
27	3033	93.0	641	2	AAY45247	Aay45247	Human	p51
28	3033	93.0	641	2	AAY05953	Aay05953	Human	cel
29	3033	93.0	641	4	AAB82129	Aab82129	Human	pro
30	3033	93.0	641	5	ABG95142	Abg95142	Human	onc
31	3033	93.0	687	7	ADL22695	Adl22695	Human	dis
32	3029	92.9	641	3	AAB11358	Aab11358	Human	p63
33	3029	92.9	641	5	ABG95136	Abg95136	Human	onc
34	3029	92.9	641	5	ABG95128	Abg95128	Human	onc
35	3029	92.9	641	5	ABB74990	Abb74990	Human	p53
36	3029	92.9	641	5	ABP61910	Abp61910	Human	lun
37	3029	92.9	641	7	ADA28429	Ada28429	p53 tumou	
38	3029	92.9	641	7	ADH36993	Adh36993	Human	lun
39	3029	92.9	641	8	ADM56796	Adm56796	Human	lun
40	3029	92.9	641	9	ADU98488	Adu98488	Human	p53
41	3029	92.9	641	9	AEB10296	Aeb10296	Cancer re	
42	3029	92.9	641	9	AEE06150	Aee06150	p53 tumor	
43	3025	92.8	680	3	AAY50997	Aay50997	Human	KET
44	3025	92.8	680	3	AAB11361	Aab11361	Human	p63
45	3025	92.8	680	5	ABB74993	Abb74993	Human	p53

&lt;!--EndFragment--&gt;

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: December 27, 2006, 19:26:20 ; Search time 107.5 Seconds  
(without alignments)  
4545.914 Million cell updates/sec

Title: US-10-716-359-4  
Perfect score: 3260  
Sequence: 1 atgttggtacctggaaaacaa.....tcaaagaggaggggggagtga 1761

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 5699196

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10716359/runat\_27122006\_140407\_336/app\_query.fasta\_1  
-DB=UniProt -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p  
-USER=US10716359@CGN\_1\_1\_891@runat\_27122006\_140407\_336 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3033	93.0	680	1	P73L_HUMAN	Q9h3d4 homo sapien
2	3026	92.8	582	2	Q3UVI3_MOUSE	Q3uvi3 mus musculu
3	3017	92.5	582	2	Q5CZX0_MOUSE	Q5czx0 mus musculu
4	2995	91.9	680	1	P73L_MOUSE	O88898 mus musculu
5	2991	91.7	680	1	P73L_RAT	Q9jpp6 rattus norv
6	2962	90.9	582	2	Q9DEC7_CHICK	Q9dec7 gallus gall
7	2416	74.1	565	2	Q4S122_TETNG	Q4s122 tetraodon n
8	2344	71.9	576	2	Q8JFE3_BRARE	Q8jfe3 brachydanio

9	2330	71.5	588	2	Q8JHZ6_BRARE	Q8jhz6 brachydanio
10	1877	57.6	393	2	Q569E5_MOUSE	Q569e5 mus musculu
11	1826	56.0	457	2	Q8JHZ5_BRARE	Q8jhz5 brachydanio
12	1777	54.5	641	2	Q9W664_BARBU	Q9w664 barbus barb
13	1774	54.4	640	2	Q801Z7_BRARE	Q801z7 brachydanio
14	1771	54.3	640	2	Q6UNX2_BRARE	Q6unx2 brachydanio
15	1748.5	53.6	590	2	Q9JJP1_MOUSE	Q9jjp1 mus musculu
16	1744.5	53.5	631	2	Q9JJP2_MOUSE	Q9jjp2 mus musculu
17	1741	53.4	636	1	P73_HUMAN	O15350 homo sapien
18	1730.5	53.1	365	2	Q98SW0_XENLA	Q98sw0 xenopus lae
19	1720.5	52.8	637	1	P73_CERAE	Q9xsk8 cercopithec
20	1649.5	50.6	434	2	Q6DG24_BRARE	Q6dg24 brachydanio
21	1562	47.9	514	2	Q9CU77_MOUSE	Q9cu77 mus musculu
22	1507.5	46.2	494	2	Q3UT91_MOUSE	Q3ut91 mus musculu
23	1481	45.4	662	2	Q4S837_TETNG	Q4s837 tetraodon n
24	1464	44.9	555	2	Q5KQU6_BRARE	Q5kqu6 brachydanio
25	1459.5	44.8	497	2	Q9WUJ0_MOUSE	Q9wuj0 mus musculu
26	950.5	29.2	621	2	Q9NGC7_MYAAR	Q9ngc7 mya arenari
27	912	28.0	591	2	Q8T7V3_SPISO	Q8t7v3 spisula sol
28	912	28.0	596	2	Q6WG19_SPISO	Q6wg19 spisula sol
29	912	28.0	596	2	Q6WG20_SPISO	Q6wg20 spisula sol
30	898.5	27.6	564	2	Q27937_LOLFO	Q27937 loligo forb



&lt;!--StartFragment--&gt;

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: December 27, 2006, 19:36:35 ; Search time 13.3 Seconds  
(without alignments)  
3821.903 Million cell updates/sec

Title: US-10-716-359-4  
Perfect score: 3260  
Sequence: 1 atgttggtacctggaaaacaa.....tcaaagaggaggggggagtga 1761

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10716359/runat\_27122006\_140410\_379/app\_query.fasta\_1  
-DB=PIR -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p  
-USER=US10716359@CGN\_1\_1\_92@runat\_27122006\_140410\_379 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1774	54.4	640	2 JC7989	p73 protein - zebr
2	839.5	25.8	396	1 JH0631	cellular tumor ant
3	773.5	23.7	367	1 S02193	cellular tumor ant
4	762	23.4	363	1 A29376	cellular tumor ant
5	747.5	22.9	386	1 S51648	cellular tumor ant
6	736.5	22.6	391	1 S02192	cellular tumor ant

7	726	22.3	393	1	DNHU53	cellular tumor ant
8	719.5	22.1	393	1	S06594	cellular tumor ant
9	712	21.8	396	1	JH0633	cellular tumor ant
10	709.5	21.8	390	1	DNMS53	cellular tumor ant
11	701.5	21.5	391	2	JC6193	tumor suppressor p
12	697.5	21.4	393	2	JC6176	tumor suppressor p
13	692.5	21.2	381	2	S38824	cellular tumor ant
14	259.5	8.0	77	2	I46226	cellular tumor ant
15	161	4.9	925	2	T19361	hypothetical prote
16	152.5	4.7	3570	2	T45025	mucin MUC5B, trach
17	151.5	4.6	3020	2	A43932	mucin 2 precursor,
18	151	4.6	2715	2	T13049	eyelid - fruit fly
19	150	4.6	1006	2	T42731	atrophin-1 related
20	150	4.6	1188	2	S49915	extensin-like prot
21	147.5	4.5	620	2	S06733	hydroxyproline-ric
22	144.5	4.4	862	2	B53689	homeotic protein C
23	142.5	4.4	2359	2	T03094	A-kinase anchor pr
24	140.5	4.3	1199	2	A40670	nuclear envelope p
25	140.5	4.3	2232	2	T34434	hypothetical prote
26	140	4.3	847	2	F96531	hypothetical prote
27	139	4.3	1285	2	T14171	ataxin-2 - mouse
28	139	4.3	1613	2	S39059	protein BRG1 - hum
29	138	4.2	1510	2	T33100	hypothetical prote
30	136	4.2	400	2	S58222	PQ-rich protein -
31	136	4.2	650	2	T04487	hypothetical prote
32	135.5	4.2	891	2	G84693	probable proline-r
33	135.5	4.2	2649	2	T51023	hypothetical prote
34	135	4.1	975	2	S33121	homeotic protein C
35	135	4.1	1240	2	JC5209	insulin receptor s
36	135	4.1	1242	2	JS0670	insulin receptor s
37	134.5	4.1	628	2	JQ0110	hypothetical 69K p
38	134.5	4.1	901	2	JC6093	dead ringer nuclea
39	134	4.1	1520	1	TVFFA	protein-tyrosine k
40	134	4.1	1791	2	T24089	hypothetical prote
41	133.5	4.1	477	2	T46304	hypothetical prote
42	133.5	4.1	964	2	T41547	hypothetical prote
43	133	4.1	817	2	S51342	verprolin - yeast
44	133	4.1	1054	2	T43226	translation initia
45	133	4.1	1081	2	S66736	transcription acti

&lt;!--EndFragment--&gt;

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: December 27, 2006, 19:54:31 ; Search time 12.8 Seconds  
(without alignments)  
3612.690 Million cell updates/sec

Title: US-10-716-359-4  
Perfect score: 3260  
Sequence: 1 atgttggtacctggaaaacaa.....tcaaagaggagggggagtga 1761

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 1301182

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10716359/runat\_27122006\_140412\_434/app\_query.fasta\_1  
-DB=Issued\_Patents\_AA -QFMT=fastan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss02p -USER=US10716359\_@CGN\_1\_1\_84\_@runat\_27122006\_140412\_434 -NCPU=6  
-ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3104	95.2	586	2	US-09-538-106-16 Sequence 16, Appl
2	3104	95.2	586	3	US-09-529-583-16 Sequence 16, Appl
3	3087	94.7	586	2	US-09-643-597-338 Sequence 338, App

4	3087	94.7	586	2	US-09-542-615A-338	Sequence 338, App
5	3087	94.7	586	2	US-09-606-421B-338	Sequence 338, App
6	3087	94.7	586	2	US-09-630-940B-338	Sequence 338, App
7	3087	94.7	586	2	US-10-007-700-338	Sequence 338, App
8	3080	94.5	586	2	US-09-643-597-152	Sequence 152, App
9	3080	94.5	586	2	US-09-480-884A-152	Sequence 152, App
10	3080	94.5	586	2	US-09-542-615A-152	Sequence 152, App
11	3080	94.5	586	2	US-09-606-421B-152	Sequence 152, App
12	3080	94.5	586	2	US-09-221-107-152	Sequence 152, App
13	3080	94.5	586	2	US-09-466-396A-152	Sequence 152, App
14	3080	94.5	586	2	US-09-476-496A-152	Sequence 152, App
15	3080	94.5	586	2	US-09-630-940B-152	Sequence 152, App
16	3080	94.5	586	2	US-09-285-479-152	Sequence 152, App
17	3080	94.5	586	2	US-10-007-700-152	Sequence 152, App
18	3066	94.0	586	2	US-09-538-106-22	Sequence 22, Appl
19	3066	94.0	586	3	US-09-529-583-22	Sequence 22, Appl
20	3033	93.0	641	2	US-09-538-106-13	Sequence 13, Appl
21	3033	93.0	641	3	US-09-529-583-13	Sequence 13, Appl
22	3029	92.9	641	2	US-09-643-597-339	Sequence 339, App
23	3029	92.9	641	2	US-09-542-615A-339	Sequence 339, App
24	3029	92.9	641	2	US-09-606-421B-339	Sequence 339, App
25	3029	92.9	641	2	US-09-630-940B-339	Sequence 339, App
26	3029	92.9	641	2	US-10-007-700-339	Sequence 339, App
27	3025	92.8	680	2	US-09-643-597-342	Sequence 342, App
28	3025	92.8	680	2	US-09-542-615A-342	Sequence 342, App
29	3025	92.8	680	2	US-09-606-421B-342	Sequence 342, App
30	3025	92.8	680	2	US-09-630-940B-342	Sequence 342, App
31	3025	92.8	680	2	US-10-007-700-342	Sequence 342, App
32	2995	91.9	680	2	US-09-538-106-19	Sequence 19, Appl
33	2995	91.9	680	3	US-09-529-583-19	Sequence 19, Appl
34	2421	74.3	461	2	US-09-643-597-343	Sequence 343, App
35	2421	74.3	461	2	US-09-542-615A-343	Sequence 343, App
36	2421	74.3	461	2	US-09-606-421B-343	Sequence 343, App
37	2421	74.3	461	2	US-09-630-940B-343	Sequence 343, App
38	2421	74.3	461	2	US-09-538-106-17	Sequence 17, Appl
39	2421	74.3	461	2	US-10-007-700-343	Sequence 343, App
40	2421	74.3	461	3	US-09-529-583-17	Sequence 17, Appl
41	2398	73.6	461	2	US-09-538-106-23	Sequence 23, Appl
42	2398	73.6	461	3	US-09-529-583-23	Sequence 23, Appl
43	2350	72.1	516	2	US-09-643-597-344	Sequence 344, App
44	2350	72.1	516	2	US-09-542-615A-344	Sequence 344, App
45	2350	72.1	516	2	US-09-606-421B-344	Sequence 344, App

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: December 27, 2006, 20:28:36 ; Search time 58.9 Seconds  
(without alignments)  
4154.778 Million cell updates/sec

Title: US-10-716-359-4  
Perfect score: 3260  
Sequence: 1 atgttggtacctggaaaacaa.....tcaaagaggagggggagtga 1761

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 4195594

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+\_n2p.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10716359/runat\_27122006\_140422\_629/app\_query.fasta\_1  
-DB=Published\_Applications\_AA\_Main -QFMT=fastan -SUFFIX=n2p.rapbm  
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1  
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext  
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p  
-USER=US10716359\_CGN\_1\_1\_446\_@runat\_27122006\_140422\_629 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3104	95.2	586	4	US-10-716-359-16 Sequence 16, Appl
2	3104	95.2	586	5	US-10-469-469-306 Sequence 306, App
3	3104	95.2	586	6	US-11-109-831-16 Sequence 16, Appl

4	3100	95.1	586	5	US-10-469-469-290	Sequence 290, App
5	3087	94.7	586	3	US-09-735-705-338	Sequence 338, App
6	3087	94.7	586	3	US-09-850-716A-338	Sequence 338, App
7	3087	94.7	586	3	US-09-897-778-338	Sequence 338, App
8	3087	94.7	586	4	US-10-007-700-338	Sequence 338, App
9	3087	94.7	586	4	US-10-117-982-338	Sequence 338, App
10	3087	94.7	586	4	US-10-313-986-338	Sequence 338, App
11	3087	94.7	586	5	US-10-775-972-338	Sequence 338, App
12	3087	94.7	586	5	US-10-922-124-338	Sequence 338, App
13	3087	94.7	586	5	US-10-623-155-338	Sequence 338, App
14	3080	94.5	586	3	US-09-735-705-152	Sequence 152, App
15	3080	94.5	586	3	US-09-850-716A-152	Sequence 152, App
16	3080	94.5	586	3	US-09-897-778-152	Sequence 152, App
17	3080	94.5	586	3	US-09-466-396A-152	Sequence 152, App
18	3080	94.5	586	4	US-10-007-700-152	Sequence 152, App
19	3080	94.5	586	4	US-10-117-982-152	Sequence 152, App
20	3080	94.5	586	4	US-10-313-986-152	Sequence 152, App
21	3080	94.5	586	5	US-10-775-972-152	Sequence 152, App
22	3080	94.5	586	5	US-10-922-124-152	Sequence 152, App
23	3080	94.5	586	5	US-10-623-155-152	Sequence 152, App
24	3066	94.0	586	4	US-10-716-359-22	Sequence 22, Appl
25	3066	94.0	586	6	US-11-109-831-22	Sequence 22, Appl
26	3033	93.0	641	4	US-10-716-359-13	Sequence 13, Appl
27	3033	93.0	641	5	US-10-469-469-310	Sequence 310, App
28	3033	93.0	641	6	US-11-109-831-13	Sequence 13, Appl
29	3029	92.9	641	3	US-09-735-705-339	Sequence 339, App
30	3029	92.9	641	3	US-09-850-716A-339	Sequence 339, App
31	3029	92.9	641	3	US-09-897-778-339	Sequence 339, App
32	3029	92.9	641	4	US-10-007-700-339	Sequence 339, App
33	3029	92.9	641	4	US-10-117-982-339	Sequence 339, App
34	3029	92.9	641	4	US-10-313-986-339	Sequence 339, App
35	3029	92.9	641	5	US-10-775-972-339	Sequence 339, App
36	3029	92.9	641	5	US-10-922-124-339	Sequence 339, App
37	3029	92.9	641	5	US-10-623-155-339	Sequence 339, App
38	3029	92.9	641	5	US-10-469-469-282	Sequence 282, App
39	3029	92.9	641	5	US-10-469-469-298	Sequence 298, App
40	3025	92.8	680	3	US-09-735-705-342	Sequence 342, App
41	3025	92.8	680	3	US-09-850-716A-342	Sequence 342, App
42	3025	92.8	680	3	US-09-897-778-342	Sequence 342, App
43	3025	92.8	680	4	US-10-007-700-342	Sequence 342, App
44	3025	92.8	680	4	US-10-117-982-342	Sequence 342, App
45	3025	92.8	680	4	US-10-313-986-342	Sequence 342, App

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: December 27, 2006, 20:35:01 ; Search time 13.7 Seconds  
(without alignments)  
3773.012 Million cell updates/sec

Title: US-10-716-359-4  
Perfect score: 3260  
Sequence: 1 atgttggtacctggaaaacaa.....tcaaagaggagggggagtga 1761

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 390055 seqs, 97842647 residues

Total number of hits satisfying chosen parameters: 780110

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10716359/runat\_27122006\_140426\_732/app\_query.fasta\_1  
-DB=Published\_Applications\_AA\_New -QFMT=fastan -SUFFIX=n2p.rapbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abss02p  
-USER=US10716359\_CGN\_1\_1\_94\_@runat\_27122006\_140426\_732 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	3033	93.0	641	7 US-11-340-715-4	Sequence 4, Appli

2	2995	91.9	641	7	US-11-340-715-11	Sequence 11, Appl
3	1813	55.6	448	7	US-11-340-715-1	Sequence 1, Appli
4	1746	53.6	587	6	US-10-489-730-2	Sequence 2, Appli
5	1741	53.4	636	7	US-11-340-715-8	Sequence 8, Appli
6	1718.5	52.7	661	6	US-10-489-730-11	Sequence 11, Appl
7	1420.5	43.6	450	6	US-10-489-730-4	Sequence 4, Appli
8	1415.5	43.4	499	7	US-11-340-715-6	Sequence 6, Appli
9	1293.5	39.7	426	6	US-10-489-730-6	Sequence 6, Appli
10	1046	32.1	312	7	US-11-340-715-7	Sequence 7, Appli
11	960.5	29.5	349	7	US-11-340-715-9	Sequence 9, Appli
12	726	22.3	393	7	US-11-340-715-3	Sequence 3, Appli
13	726	22.3	393	7	US-11-009-357-6	Sequence 6, Appli
14	726	22.3	425	7	US-11-009-357-2	Sequence 2, Appli
15	721	22.1	393	6	US-10-546-829-1	Sequence 1, Appli
16	719	22.1	393	6	US-10-538-066-367	Sequence 367, App
17	719	22.1	393	7	US-11-315-777-9	Sequence 9, Appli
18	719	22.1	393	7	US-11-319-873-9	Sequence 9, Appli
19	719	22.1	393	7	US-11-254-926-9	Sequence 9, Appli
20	719	22.1	393	7	US-11-304-280-9	Sequence 9, Appli
21	719	22.1	393	7	US-11-239-548-9	Sequence 9, Appli
22	718	22.0	393	7	US-11-371-354-72585	Sequence 72585, A
23	714	21.9	393	7	US-11-404-146-3	Sequence 3, Appli
24	713	21.9	354	6	US-10-538-066-763	Sequence 763, App
25	316	9.7	102	6	US-10-538-066-765	Sequence 765, App
26	291.5	8.9	100	6	US-10-489-730-12	Sequence 12, Appl
27	285.5	8.8	100	6	US-10-489-730-14	Sequence 14, Appl
28	284.5	8.7	100	6	US-10-489-730-13	Sequence 13, Appl
29	163	5.0	2240	6	US-10-544-731-4	Sequence 4, Appli
30	163	5.0	2258	6	US-10-544-731-3	Sequence 3, Appli
31	163	5.0	2264	6	US-10-544-731-5	Sequence 5, Appli
32	154.5	4.7	634	7	US-11-293-697-3340	Sequence 3340, Ap
33	149.5	4.6	693	7	US-11-293-697-3849	Sequence 3849, Ap
34	143.5	4.4	1113	7	US-11-056-355B-77057	Sequence 77057, A
35	142.5	4.4	1690	6	US-10-516-780-28	Sequence 28, Appl
36	141	4.3	690	6	US-10-449-902-41507	Sequence 41507, A
37	140.5	4.3	312	6	US-10-953-349-31493	Sequence 31493, A
38	140.5	4.3	312	7	US-11-056-355B-68325	Sequence 68325, A
39	140	4.3	691	7	US-11-056-355B-79590	Sequence 79590, A
40	140	4.3	718	7	US-11-056-355B-79589	Sequence 79589, A
41	140	4.3	847	7	US-11-056-355B-79588	Sequence 79588, A
42	138.5	4.2	5178	6	US-10-700-439-178	Sequence 178, App
43	138.5	4.2	5179	6	US-10-541-749-151	Sequence 151, App
44	138.5	4.2	5179	7	US-11-105-233-185	Sequence 185, App
45	138	4.2	934	6	US-10-449-902-41077	Sequence 41077, A